

1643

BATCH

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/367,052

DATE: 01/05/2000
 TIME: 13:10:51

Input Set: I367052.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

J.S
ENTERED

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1 <110> APPLICANT: KISHIMOTO, Tadamitsu
2 NAGASAWA, Takashi
3 TACHIBANA, Kazunobu
4 IIZASA, Hisashi
5 YOSHIDA, Nobuaki
6 NAKAJIMA, Toshihiro
7 YOSHIE, Osamu
8 <120> TITLE OF INVENTION: NOVEL MOUSE CXC CHEMOKINE RECEPTOR
9 <130> FILE REFERENCE: 1422-386P
10 <140> CURRENT APPLICATION NUMBER: US/09/367,052
11 <141> CURRENT FILING DATE: 1999-08-06
12 <160> NUMBER OF SEQ ID NOS: 22
13 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO 1
15 <211> LENGTH: 1877
16 <212> TYPE: DNA
17 <213> ORGANISM: Mus sp.
18 <220> FEATURE:
19 <221> NAME/KEY: CDS
20 <222> LOCATION: (120)..(1196)
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23 tgaccctctg aggcgtttgg tgctccggta accaccacgg ctgttagagcg agtgttgcc 119
24 atg gaa ccg atc agt gtg agt ata tac, act tct gat aac tac tct gaa 167
25 Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu
26 1 5 10 15
27 gaa gtg ggg tct gga gac tat gac tcc aac aag gaa ccc tgc ttc cgg 215
28 Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
29 20 25 30
30 gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc atc tac ttc 263
31 Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
32 35 40 45
33 atc atc ttc ttg act ggc ata gtc ggc aat gga ttg gtg atc ctg gtc 311
34 Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
35 50 55 60
36 atg ggt tac cag aag aag cta agg agc atg acg gac aag tac cgg ctg 359
37 Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
38 65 70 75 80
39 cac ctg tca gtg gct gac ctc ctc ttt gtc atc aca ctc ccc ttc tgg 407
40 His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
41 85 90 95
42 gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt aag 455
43 Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
44 100 105 110

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45 gct gtc cat atc atc tac act gtc aac ctc tac agc agc gtt ctc atc 503
 46 Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
 47 115 120 125
 48 ctg gcc ttc atc agc ctg gac cggttccatcgttccattgtcacggacc 551
 49 Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
 50 130 135 140
 51 aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat gtg 599
 52 Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
 53 145 150 155 160
 54 ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc ttt 647
 55 Gly Val Trp Ile Pro Ala Leu Leu Thr Ile Pro Asp Phe Ile Phe
 56 165 170 175
 57 gcc gac gtc agc cag ggg gac atc agt cag ggg gat gac agg tac atc 695
 58 Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
 59 180 185 190
 60 tgt gac cgc ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc 743
 61 Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
 62 195 200 205
 63 cag cat ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc 791
 64 Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
 65 210 215 220
 66 tgt tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag 839
 67 Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
 68 225 230 235 240
 69 aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc ttt 887
 70 Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
 71 245 250 255
 72 gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc atc 935
 73 Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
 74 260 265 270
 75 ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg cac 983
 76 Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
 77 275 280 285
 78 aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc ctg 1031
 79 Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
 80 290 295 300
 81 aac ccc atc ctc tat gcc ttc ctc ggg gcc aag ttc aaa agc tct gcc 1079
 82 Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
 83 305 310 315 320
 84 cag cat gca ctc aac tcc atg agc aga ggc tcc agc ctc aag atc ctt 1127
 85 Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
 86 325 330 335
 87 tcc aaa gga aag cgg ggt gga cac tct tcc gtc tcc acg gag tca gaa 1175
 88 Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
 89 340 345 350
 90 tcc tcc agt ttt cac tcc agc taacccttat gcaaagactt atataatata 1226
 91 Ser Ser Ser Phe His Ser Ser
 92 355
 93 tatatatata tgataaaagaa cttttttatg ttacacattt tccagatata agagactgac 1286
 94 cagtcttgta cagttttttt tttttttaa ttgactgttg ggagttatg ttcctctagt 1346

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96      gcgtctaggc aggacctgtg gccaagttct tagtagctgt ttatctgtgt gttaggactgt 1466
97      agaactgttag aggaagaaac tgaacattcc agaatgtgtg gtaaattgaa taaagctagc 1526
98      cgtgatccctc agctgttgct gcataatctc ttcattccga ggagcacccc acccccaccc 1586
99      ccaccccccac cccattctta aattgtttgg ttatgctgtg tgatggttt tttgggtttt 1646
100     ttttgttgg ttttttctg taaaagatgg cacttaaaac caaagcctga 1706
101     aatgggtgta gaaatgctgg ggttttttt gtttgggtt ttttcagtt ttcaagagta 1766
102     gattgacttc agtccctaca aatgtacagt cttgtattac attgttaata aaagtcaatg 1826
103     ataaacttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 1877
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105 <211> LENGTH: 359
106 <212> TYPE: PRT
107 <213> ORGANISM: Mus sp.
108 <400> SEQUENCE: 2
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111     Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
112           20            25            30
113     Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
114           35            40            45
115     Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val
116           50            55            60
117     Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu
118           65            70            75            80
119     His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp
120           85            90            95
121     Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
122           100           105           110
123     Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile
124           115           120           125
125     Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr
126           130           135           140
127     Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val
128           145           150           155           160
129     Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe
130           165           170           175
131     Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile
132           180           185           190
133     Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe
134           195           200           205
135     Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser
136           210           215           220
137     Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
138           225           230           235           240
139     Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
140           245           250           255
141     Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile
142           260           265           270
143     Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His
144           275           280           285

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145 Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu
 146 290 295 300
 147 Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala
 148 305 310 315 320
 149 Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu
 150 325 330 335
 151 Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
 152 340 345 350
 153 Ser Ser Ser Phe His Ser Ser
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 155 <210> SEQ ID NO 3
 156 <211> LENGTH: 690
 157 <212> TYPE: DNA
 158 <213> ORGANISM: Mus sp.
 159 <220> FEATURE:
 160 <221> NAME/KEY: CDS
 161 <222> LOCATION: (1)...(690)
 162 <400> SEQUENCE: 3

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1 5 10 15	
tgg gca gtt gat gcc atg gct gac tgg tac ttt ggg aaa ttt ttg tgt	96
Trp Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys	
20 25 30	
aag gct gtc cat atc atc tac act gtc aac ctc tac agc agc gtt ctc	144
Lys Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu	
35 40 45	
atc ctg gcc ttc atc agc ctg gac cgg tac ctc gcc att gtc cac gcc	192
Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala	
50 55 60	
acc aac agt caa agg cca agg aaa ctg ctg gct gaa aag gca gtc tat	240
Thr Asn Ser Gln Arg Pro Arg Lys Leu Ala Glu Lys Ala Val Tyr	
65 70 75 80	
gtg ggc gtc tgg atc cca gcc ctc ctc ctg act ata cct gac ttc atc	288
Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile	
85 90 95	
ttt gcc gac gtc agc cag ggg gac atc agt cag ggg gat gac agg tac	336
Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr	
100 105 110	
atc tgt gac cgc ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa	384
Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln	
115 120 125	
ttc cag cat ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc	432
Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu	
130 135 140	
tcc tgt tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac	480
Ser Cys Tyr Cys Ile Ile Ser Lys Leu Ser His Ser Lys Gly His	
145 150 155 160	
cag aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc	528
Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe	

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195	165	170	175
196	ttt gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc		576
197	Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe		
198	180	185	190
199	atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg		624
200	Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val		
201	195	200	205
202	cac aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc		672
203	His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys		
204	210	215	220
205	ctg aac ccc atc ctc tat		690
206	Leu Asn Pro Ile Leu Tyr		
207	225	230	
208	<210> SEQ ID NO 4		
209	<211> LENGTH: 230		
210	<212> TYPE: PRT		
211	<213> ORGANISM: Mus sp.		
212	<400> SEQUENCE: 4		
213	Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe		
214	1	5	10
215	Trp Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys		
216	20	25	30
217	Lys Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu		
218	35	40	45
219	Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala		
220	50	55	60
221	Thr Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr		
222	65	70	75
223	Val Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile		
224	85	90	95
225	Phe Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr		
226	100	105	110
227	Ile Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln		
228	115	120	125
229	Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu		
230	130	135	140
231	Ser Cys Tyr Cys Ile Ile Ser Lys Leu Ser His Ser Lys Gly His		
232	145	150	155
233	Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe		
234	165	170	175
235	Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe		
236	180	185	190
237	Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val		
238	195	200	205
239	His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys		
240	210	215	220
241	Leu Asn Pro Ile Leu Tyr		
242	225	230	
243	<210> SEQ ID NO 5		
	<211> LENGTH: 685		

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



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VERIFICATION SUMMARY
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DATE: 01/05/2000

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Input Set: I367052.RAW

Line ? Error/Warning

Original Text

467 W "N" or "Xaa" used: Feature required

ctsmgttgk cmntnkcyga

483 W "N" or "Xaa" used: Feature required

tagaksanng grttsanrca rcagtg